

AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** A method for identifying and/or quantifying an organism or part of an organism ~~by a detecting its nucleotide sequence among at least 4 other homologous sequences in a sample by detecting a nucleotide sequence characteristic of said organism, wherein said nucleotide sequence is homologous to at least 4 other nucleotide sequences from other organisms~~ comprising:

~~a. extracting original nucleotide sequences from the organism;~~

~~b. amplifying or copying with a unique pair of primers, at least part of original said nucleotide sequences into target nucleotide sequences to be detected~~ **using primer pairs which are capable of amplifying at least two of said homologous nucleotide sequences from other organisms;**

~~c. labelling said target nucleotide sequences;~~

~~d. contacting said amplified or copied~~ **putting into contact the labelled target nucleotide sequences with single-stranded capture nucleotide sequences, said single-stranded capture nucleotide sequences being bound by a single predetermined link in an array to an insoluble solid support, preferably a non porous via a spacer which is at least 6.8 nm in length, wherein said array comprises at least 4 different bound single-stranded capture nucleotide sequences/cm² of solid support,— surface and wherein said capture nucleotide sequences comprise a nucleotide sequence of about 10 to about 60 bases which is able to specifically bind to said target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences; and**

~~e. discriminating the binding of a target nucleotide sequence detecting specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the of said target nucleotide sequence to said and its corresponding capture nucleotide sequences;~~

~~wherein said capture nucleotide sequence being bound to the insoluble solid support at a specific location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and~~

~~wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms results in said signal at the expected location, the detection of a single~~

signal allowing a discrimination of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences.

2. **(Currently amended)** The method according to claim 1, wherein the amplified ~~homologous original~~ nucleotide sequence is a DNA nucleotide sequence.

3. **(Canceled)**

4. **(Currently amended)** The method according to claim 1, wherein the amplified ~~homologous original~~ nucleotide sequences are mRNA first ~~retrotranscribed~~ reverse transcribed into cDNA with the same primer pair and then amplified using said primer pair which is capable of amplifying at least two of said homologous mRNA in said sample.

5-7. **(Canceled)**

8. **(Currently amended)** The method according to the claim ~~7-1~~, wherein said ~~spacer is a~~ capture nucleotide sequences comprise a nucleotide sequence of between about 15 and about 40 bases which is able to specifically bind to said target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences from other organisms.

9. **(Currently amended)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is ~~superior to more than about~~ 10 fmoles and preferably 100 fmoles per cm² of solid support surface.

10. **(Currently amended)** The method according to claim 1, wherein the target nucleotide sequence ~~to be detected~~ presents ~~an a~~ homology with other homologous nucleotide sequences higher than 30%, ~~preferably higher than 60%, more preferably higher than 80%.~~

11. **(Canceled)**

12. **(Currently amended)** The method according to claim 1, ~~characterised in that~~ wherein other primers are present in the amplification step for the amplification of ~~other another~~ nucleotide sequences sequence, such as an antibiotic resistance determining sequence.

13. **(Currently amended)** The method according to claim 1, ~~characterised in that~~ wherein the insoluble solid support is selected from the group consisting of: glasses, electronic devices, silicon supports, plastic supports, compact discs, filters, filters, gel layers, and metallic supports ~~and a mixture thereof.~~

14. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ nucleotide ~~sequences~~ sequence to be detected ~~identified~~ and/or ~~be~~ quantified ~~are~~ is an RNA

~~sequences~~ sequence submitted to a ~~retro transcription~~ reverse transcription of the ~~its~~ 3' or 5' end by using a consensus primer and ~~possibly a stopper sequence~~.

15. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ nucleotide ~~sequences~~ sequence to be identified and/or quantified ~~in a sample are FemA genetic sequences~~ are from the FemA gene of Staphylococci species selected from the group consisting of: *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* ~~and/or~~ and *S. haemolyticus*.

16. **(Currently amended)** The method according to claim 1, wherein the solid support also bears capture nucleotide sequences specific of the homologous sequences specific for the binding with the homologous target nucleotide sequence together with a consensus sequence able to bind to said target nucleotide sequence and to said at least 4 homologous nucleotide sequences ~~for a common detection~~.

17. **(Original)** The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a Staphylococcus genus identification.

18. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the *MAGE* gene family.

19. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the *HLA-A* genes family.

20. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

21. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

22. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be detected and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

23. **(Currently amended)** The method according to claim 1, wherein the ~~original~~ sequence to be detected and/or quantified in the sample belongs to the cytochrome p450 forms family.

24-37. (Withdrawn).

38. (Currently amended) The method of Claim 1, wherein said nucleotide sequence to be identified and/or quantified originates from organism is a microorganism.

39. (Canceled)

40. (New) The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 100 fmoles per cm^2 of solid support surface.

41. (New) The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 60%.

42. (New) The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 80%.

43. (New) The method according to claim 1, wherein the spacer is a non-specific nucleotide sequence of at least 20 nucleotides.

44. (New) The method of Claim 12, wherein said other nucleotide sequence is an antibiotic resistance determining sequence.

45. (New) The method of Claim 1, wherein said organism is identified or quantitated by detecting a single spot signal at one specific location on said insoluble solid support.